Full wwPDB X-ray Structure Validation Report (i)

Oct 29, 2024 – 01:46 pm GMT

PDB ID	:	8RZA
Title	:	Ribonuclease W
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Deposited on	:	2024-02-12
Resolution	:	2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

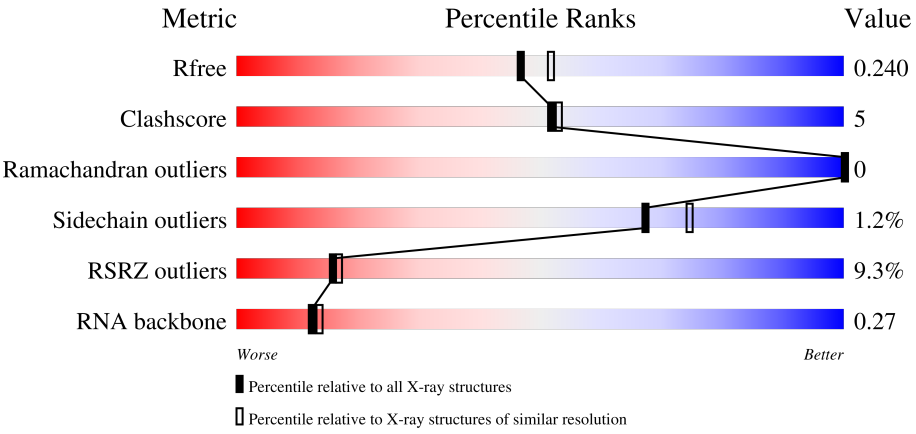
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)
RNA backbone	3690	1014 (2.46-1.74)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	469	9%, 88%, 11% .
2	R	3	67%, 33%
3	B	3	33%, 67%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4076 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Probable ribonuclease FAU-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	465	3769	2442	631	695	1	0	0	0

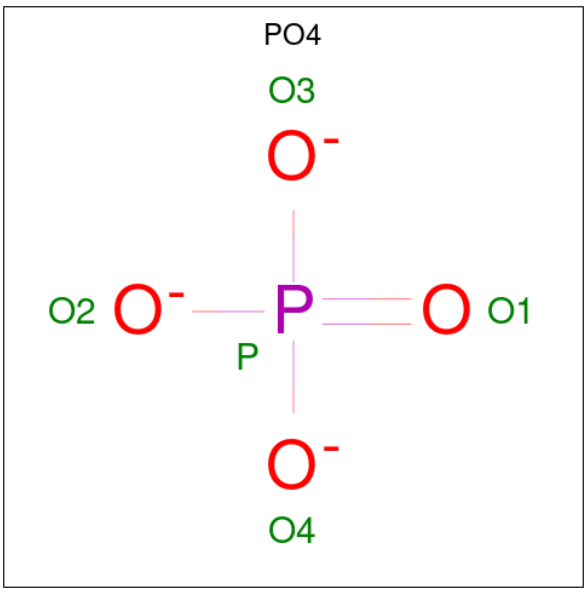
- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	R	3	45	18	4	20	3	0	0	0

- Molecule 3 is a RNA chain called RNA (5'-R(*UP*AP*U)-3').

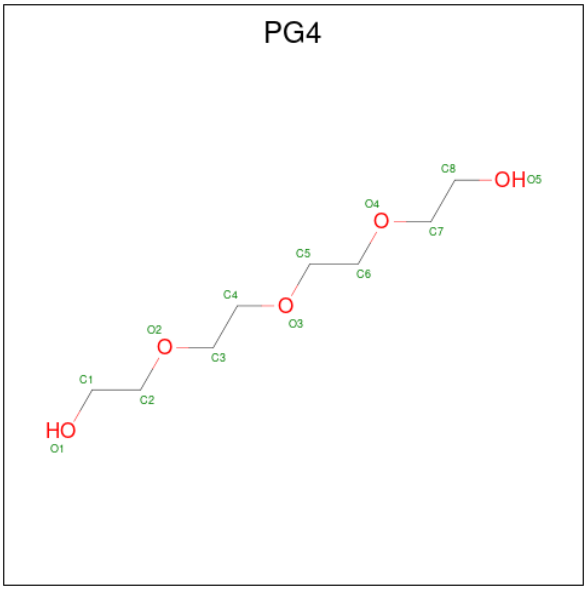
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	B	3	43	19	7	15	2	0	0	0

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 13 8 5	0	0
5	A	1	Total C O 10 6 4	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	2	Total Mg 2 2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	176	Total O 176 176	0	0
7	R	2	Total O 2 2	0	0

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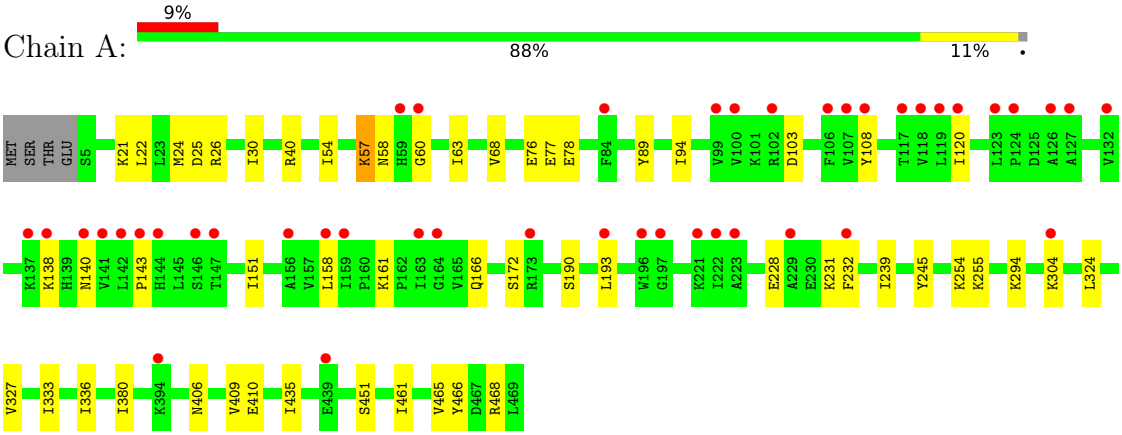
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	6	Total O 6 6	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Probable ribonuclease FAU-1



• Molecule 2: RNA (5'-R(P*UP*UP*U)-3')

• Molecule 3: RNA (5'-R(*UP*AP*U)-3')

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α, β, γ	120.62Å 120.62Å 93.84Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.64 – 2.10 45.64 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.64-2.10) 100.0 (45.64-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.31 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.212 , 0.244 0.209 , 0.240	Depositor DCC
R_{free} test set	2318 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	47.2	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 49.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4076	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PO4, PG4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.37	0/3851	0.54	1/5205 (0.0%)
2	R	1.22	1/48 (2.1%)	0.98	0/71
3	B	0.93	0/47	1.85	0/72
All	All	0.40	1/3946 (0.0%)	0.58	1/5348 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	1	U	OP3-P	-7.58	1.52	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	57	LYS	N-CA-C	-6.34	93.89	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3769	0	3845	36	0
2	R	45	0	20	1	0
3	B	43	0	22	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	10	0	0	0	0
5	A	23	0	31	5	0
6	A	2	0	0	0	0
7	A	176	0	0	5	0
7	B	6	0	0	0	0
7	R	2	0	0	0	0
All	All	4076	0	3918	39	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:LYS:HG3	1:A:58:ASN:H	1.31	0.95
1:A:54:ILE:HG12	1:A:63:ILE:HD13	1.53	0.88
1:A:228:GLU:HB3	1:A:231:LYS:HG2	1.60	0.82
1:A:255:LYS:NZ	7:A:603:HOH:O	2.27	0.68
1:A:63:ILE:HG22	1:A:68:VAL:HG22	1.80	0.62
1:A:57:LYS:CG	1:A:58:ASN:H	2.09	0.62
1:A:57:LYS:HG3	1:A:58:ASN:N	2.10	0.61
1:A:22:LEU:HD11	1:A:78:GLU:HG3	1.87	0.57
1:A:68:VAL:HG11	1:A:245:TYR:CD1	2.40	0.56
1:A:57:LYS:HG2	1:A:60:GLY:C	2.27	0.55
1:A:103:ASP:O	1:A:120:ILE:HD11	2.09	0.53
1:A:327:VAL:HG22	1:A:333:ILE:HD13	1.92	0.52
1:A:26:ARG:NH2	1:A:77:GLU:OE1	2.43	0.51
1:A:76:GLU:HG2	1:A:451:SER:HB3	1.92	0.51
1:A:161:LYS:NZ	1:A:166:GLN:HA	2.26	0.49
1:A:138:LYS:HD2	7:A:643:HOH:O	2.14	0.48
1:A:193:LEU:N	7:A:606:HOH:O	2.32	0.48
1:A:435:ILE:HG13	1:A:466:TYR:CD1	2.49	0.47
3:B:2:A:O2'	3:B:3:U:OP1	2.32	0.47
1:A:151:ILE:HB	1:A:158:LEU:HB2	1.96	0.47
1:A:26:ARG:NH1	1:A:78:GLU:OE2	2.48	0.46
1:A:103:ASP:HB2	1:A:108:TYR:HE1	1.79	0.46
1:A:380:ILE:HG12	1:A:409:VAL:HG11	1.98	0.46
1:A:21:LYS:NZ	1:A:25:ASP:OD2	2.47	0.46
1:A:24:MET:HG3	1:A:30:ILE:HG12	1.98	0.45
1:A:468:ARG:HD2	5:A:503:PG4:H62	1.98	0.45
5:A:503:PG4:H82	7:A:748:HOH:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:LYS:HE2	1:A:232:PHE:CE1	2.53	0.44
5:A:503:PG4:H42	7:A:726:HOH:O	2.18	0.43
1:A:294:LYS:HD3	1:A:294:LYS:HA	1.69	0.43
1:A:465:VAL:HA	5:A:503:PG4:H61	2.01	0.42
1:A:254:LYS:HD2	1:A:410:GLU:OE2	2.19	0.42
1:A:94:ILE:HB	1:A:239:ILE:HB	2.03	0.41
1:A:161:LYS:HZ1	1:A:166:GLN:HA	1.85	0.41
1:A:324:LEU:HB2	1:A:336:ILE:HB	2.01	0.41
1:A:89:TYR:CE2	1:A:143:PRO:HB3	2.56	0.40
1:A:54:ILE:HG12	1:A:63:ILE:CD1	2.37	0.40
1:A:172:SER:HB2	2:R:1:U:H5'	2.03	0.40
1:A:461:ILE:HD11	5:A:502:PG4:H62	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	463/469 (99%)	448 (97%)	15 (3%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	407/411 (99%)	402 (99%)	5 (1%)	67 74

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	140	ASN
1	A	190	SER
1	A	304	LYS
1	A	406	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	1/3 (33%)	0	0
3	B	1/3 (33%)	0	0
All	All	2/6 (33%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	PG4	A	503	-	9,9,12	0.45	0	8,8,11	0.50	0
4	PO4	A	504	-	4,4,4	0.72	0	6,6,6	0.54	0
5	PG4	A	502	-	12,12,12	0.53	0	11,11,11	0.25	0
4	PO4	A	501	-	4,4,4	0.72	0	6,6,6	0.69	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PG4	A	503	-	-	1/7/7/10	-
5	PG4	A	502	-	-	5/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	502	PG4	O2-C3-C4-O3
5	A	502	PG4	O1-C1-C2-O2
5	A	502	PG4	C5-C6-O4-C7
5	A	502	PG4	C3-C4-O3-C5
5	A	503	PG4	O3-C5-C6-O4
5	A	502	PG4	O3-C5-C6-O4

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	503	PG4	4	0
5	A	502	PG4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	465/469 (99%)	0.64	44 (9%) 15 16	33, 52, 84, 106	0
2	R	3/3 (100%)	0.42	0 100 100	63, 63, 85, 101	0
3	B	3/3 (100%)	0.28	0 100 100	57, 57, 60, 62	0
All	All	471/475 (99%)	0.64	44 (9%) 16 17	33, 52, 85, 106	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	142	LEU	6.5
1	A	141	VAL	5.4
1	A	119	LEU	4.7
1	A	144	HIS	4.3
1	A	124	PRO	3.3
1	A	394	LYS	3.3
1	A	120	ILE	3.2
1	A	123	LEU	3.2
1	A	107	VAL	3.1
1	A	140	ASN	3.1
1	A	163	ILE	3.1
1	A	138	LYS	3.0
1	A	229	ALA	2.9
1	A	222	ILE	2.9
1	A	126	ALA	2.9
1	A	118	VAL	2.8
1	A	132	VAL	2.8
1	A	137	LYS	2.8
1	A	193	LEU	2.6
1	A	221	LYS	2.6
1	A	100	VAL	2.5
1	A	102	ARG	2.5
1	A	108	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	164	GLY	2.4
1	A	197	GLY	2.4
1	A	173	ARG	2.4
1	A	439	GLU	2.4
1	A	84	PHE	2.4
1	A	223	ALA	2.3
1	A	106	PHE	2.3
1	A	60	GLY	2.2
1	A	304	LYS	2.2
1	A	117	THR	2.2
1	A	127	ALA	2.2
1	A	232	PHE	2.2
1	A	156	ALA	2.2
1	A	147	THR	2.1
1	A	146	SER	2.1
1	A	99	VAL	2.1
1	A	143	PRO	2.1
1	A	196	TRP	2.1
1	A	158	LEU	2.0
1	A	159	ILE	2.0
1	A	59	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	PO4	A	501	5/5	0.68	0.18	62,77,80,110	0
4	PO4	A	504	5/5	0.75	0.12	73,85,93,146	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	MG	A	505	1/1	0.80	0.16	83,83,83,83	0
5	PG4	A	502	13/13	0.89	0.15	56,64,70,73	0
5	PG4	A	503	10/13	0.93	0.10	44,50,56,57	0
6	MG	A	506	1/1	0.96	0.07	43,43,43,43	0

6.5 Other polymers (i)

There are no such residues in this entry.